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Molecular and genomic characterization of an equine molluscum contagiosum-like virus

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Cases of pox-like lesions in horses and donkeys have been associated with poxviruses belonging to different genera of the family Poxviridae, including the orthopoxviruses vaccinia virus (VACV) and horsepoxvirus (HPXV), parapoxvirus (PPV) and molluscipoxvirus (MOCV). However, with the exception of VACV and HPXV, genomic characterization of the causative agents remains largely elusive with only single short genome fragments available. Here we present the first near full-length genome sequence of an equine molluscum contagiosum-like virus (eqMCLV) directly determined from skin biopsies of a horse with generalized papular dermatitis. Histopathological analysis of the lesions revealed an epidermal hyperplasia, consisting of an enlarged stratum spinosum with numerous large, eosinophilic, intracytoplasmic inclusion bodies within keratinocytes. Virions were detected in the lesions in embedded tissue by transmission electron microscopy. The genome sequence determined by next and third-generation sequencing comprises 161,270 nucleotides (nt) with inverted terminal repeats of at least 670 nt. 21 of the predicted 158 ORFs have no homologues in other poxviruses. Intriguingly, two of these ORFs were identified to encode homologues of mammalian proteins involved in immune signaling pathways, namely SECTM1 and IGFLR1, offering new insights into the vast portfolio of poxvirus immune evasion strategies. Also, IL18-binding protein seems to be acquired in an independent capture event from the host genome as the position of the poxvirus homologues differs markedly in MOCV and eqMCLV, underlining the importance of IL18 antagonists for the replication of molluscipoxviruses in the host epidermis. Phylogenetic analysis of the eqMCLV genome revealed a clear relationship to MOCV, however, with only 90 % sequence similarity in the conserved core region it should be assigned to a new species in the genus molluscipoxvirus.

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